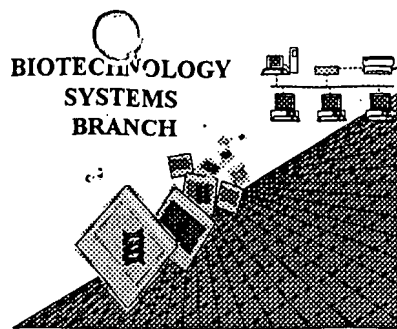


RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/265,540P
Source: 1647
Date Processed by STIC: 3/27/2001

RECEIVED

APR 04 2001

TECH CENTER 1600/2901

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/265,540D

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.
- 12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1647

RAW SEQUENCE LISTING

DATE: 03/27/2001

PATENT APPLICATION: US/09/265,540D

TIME: 10:50:04

Input Set : A:\804k.app

Output Set: N:\CRF3\03272001\I265540D.raw

Does Not Comply
Corrected Diskette Needed

see pp. 2-3, 5

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3 <110> APPLICANT: Parham, Christi L.
4   Moore, Kevin W.
5   Murgolo, Nicholas J.
6   Bazan, J. Fernando
8 <120> TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
10 <130> FILE REFERENCE: DX0804K
12 <140> CURRENT APPLICATION NUMBER: 09/265,540D
13 <141> CURRENT FILING DATE: 1999-03-08
15 <160> NUMBER OF SEQ ID NOS: 6
17 <170> SOFTWARE: PatentIn Ver. 2.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1381
21 <212> TYPE: DNA
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32   translated amino acid depends on genetic code
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35 <221> NAME/KEY: unsure
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48 <222> LOCATION: (1342)
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63 gagtctacca a atg cag act ttc aca atg gtt cta gaa gaa atc tgg aca 170
64   Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr

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RAW SEQUENCE LISTING

DATE: 03/27/2001

PATENT APPLICATION: US/09/265,540D

TIME: 10:50:04

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Output Set: N:\CRF3\03272001\I265540D.raw

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69      15          20          25
71 gat gaa gtg gcc att ctg cct gcc cct cag aac ctc tct gta ctc tca 266
72 Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
73      30          35          40          45
75 acc aac atg aag cat ctc ttg atg tgg agc cca gtg atc gcg cct gga 314
76 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly
77          50          55          60
79 gaa aca gtg tac tat tct gtc gaa tac cag ggg gag tac gag agc ctg 362
80 Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu
81          65          70          75
83 tac acg agc cac atc tgg atc ccc agc agc tgg tgc tca ctc act gaa 410
84 Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu
85          80          85          90
87 ggt cct gag tgt gat gtc act gat gac atc acg gcc act gtg cca tac 458
88 Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr
89          95          100          105
91 aac ctt cgt gtc agg gcc aca ttg ggc tca cag acc tca gcc tgg agc 506
92 Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser
93      110          115          120          125
95 atc ctg aag cat ccc ttt aat aga aac tca acc atc ctt acc cga cct 554
96 Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro
97          130          135          140
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W--> 100 Gly Met Glu Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu
101          145          150          155
103 gac ctg ggg ccc cag ttt gag ttc ctt gtg gcc tac tgg asg agg gag 650
104 Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu
105          160          165          170
107 cct ggt gcc gag gaa cat gtc aaa atg gtg agg agt ggg ggt att cca 698
108 Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro
109          175          180          185
111 gtg cac cta gaa acc atg gag cca ggg gct gca tac tgt gtg aag gcc 746
112 Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala
113      190          195          200          205
115 cag aca ttc gtg aag gcc att ggg arg tac agc gcc ttc agc cag aca 794
116 Gln Thr Phe Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr
117          210          215          220
119 gaa tgt gtg gar gtg caa gga gag gcc att ccc ctg gta ctg gcc ctg 842
120 Glu Cys Val Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu
121          225          230          235
123 ttt gcc ttt gtt ggc ttc atg ctg atc ctt gtg gtc gtg cca ctg ttc 890
124 Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe
125          240          245          250
127 gtc tgg aaa atg ggc cgg ctg ctc cag tac tcc tgt tgc ccc gtg gtg 938
128 Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val
129          255          260          265

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*move amino acids directly
under respective
codon*

RAW SEQUENCE LISTING

DATE: 03/27/2001

PATENT APPLICATION: US/09/265,540D

TIME: 10:50:04

Input Set : A:\804k.app

Output Set: N:\CRF3\03272001\I265540D.raw

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 133 270 275 280 285
 135 agc tgc aga agg gag gag gtg gat gcc tgt gcc acg gct gtg atg tct 1034
 136 Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser
 137 290 295 300
 139 cct gag gaa ctc ctc agg gcc tgg atc tca taggtttgcg gaagggccca 1084
 140 Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser
 141 305 310
 143 ggtgaagccg agaacctggt ctgcatgaca tggaaacccat gaggggacaa gttgtgtttc 1144
 145 tgttttccgc cacggacaag ggatgagaga agtaggaaga gcctgtgttc tacaagtcta 1204
 147 gaagcaacca tcagaggcag ggtggtttgt ckaacagaac aaytgactga ggytakrugg 1264
 149 gwtgtgacct ctgactktg ggstkscayt tgcwtggytg agcaagcctg ggaaaagtga 1324
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 157 <213> ORGANISM: primate
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 164 20 25 30
 166 Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser Thr Asn Met
 167 35 40 45
 169 Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val
 170 50 55 60
 172 Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu Tyr Thr Ser
 173 65 70 75 80
 175 His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu
 176 85 90 95
 178 Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg
 179 100 105 110
 181 Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys
 182 115 120 125
 184 His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu
 185 130 135 140
 W--> 187 Ile **Xaa** Lys **Xaa** Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly
 188 145 150 155 160
 W--> 190 Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp **Xaa** Arg Glu Pro Gly Ala
 191 165 170 175
 193 Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu
 194 180 185 190
 196 Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe
 197 195 200 205
 W--> 199 Val Lys Ala Ile Gly **Xaa** Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val
 200 210 215 220
 W--> 202 **Xaa** Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe
 203 225 230 235 240

all item 10 on
 Error Summary
 sheet

RAW SEQUENCE LISTING

DATE: 03/27/2001

PATENT APPLICATION: US/09/265,540D

TIME: 10:50:04

Input Set : A:\804k.app

Output Set: N:\CRF3\03272001\I265540D.raw

205 Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp Lys
 206 245 250 255
 208 Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val Leu Pro
 209 260 265 270
 211 Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Arg
 212 275 280 285
 214 Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser Pro Glu Glu
 215 290 295 300
 217 Leu Leu Arg Ala Trp Ile Ser
 218 305 310
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 236 Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro
 237 1 5 10 15
 239 tgg ttc ctg tcc tgt tgg aat gtt acc att ggg cct cct gag agc atc 97
 240 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile
 241 20 25 30
 243 tgg gtg acg ccg gga gaa gcc tcc ctc atc atc agg ttc tcc tct ccc 145
 244 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
 245 35 40 45
 247 ttc gac gtc cct ccc aac ctg ggc tat ttc cag tac tat gtc cat tay 193
 248 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His xaa
 249 50 55 60
 251 tgg gaa aag gcg gga atc caa aag gtt aaa ggt cct ttc aag agc aac 241
 252 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn
 253 65 70 75 80
 255 tcc atc gtg ttg gat ggc ttg aga ccc tta aga gaa tac tgt tta caa 289
 256 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
 257 85 90 95
 259 gtg aag gcg cat ctc ttt cgc aca tcc tgc aac acc tct agg ccc ggc 337
 260 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
 261 100 105 110
 263 cgc tta agc aac ata act tgc tac gaa aca atg atg gat gcc act acg 385
 264 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
 265 115 120 125
 267 aag ctt caa caa gtc atc ctc atc gcc gtg gga gtc ttt ctg tcg ctg 433
 268 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
 269 130 135 140
 271 gcg gcg ctg gcg ggg ggc tgt ttc ttc ctg gtg ctg aga tac aaa ggc 481

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/265,540D

DATE: 03/27/2001

TIME: 10:50:04

Input Set : A:\804k.app

Output Set: N:\CRF3\03272001\I265540D.raw

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272 Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly
273 145 150 155 160
275 ctg gtg aaa tac tgg ttt cac tct ccg cca agc atc cca tca caa atc 529
276 Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile
277 165 170 175
279 gaa gag tat ctg aag gac ccg agc cag cct atc cta gag gcc ctg gac 577
280 Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp
281 180 185 190
283 aag gac acg tca cca aca gat gat gcc tgg gac ttg gtg tct gtt gtt 625
284 Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val
285 195 200 205
287 gca ttt cca gca aag gag caa gaa gat gtt ccc caa agc act ttg acc 673
288 Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr
289 210 215 220
291 caa aac tct ggt gcg gtc tgc tagcctgtgg ggtaagggt ctgagccgag 724
292 Gln Asn Ser Gly Ala Val Cys
293 225 230
295 gaagctgctg atgtccatgt cagcacttta tggaatccgg tcctccattt tcctgtcccc 784
297 aaaaggcccg tcagtgccgt tgaagatgta acgggtctca tgggggcgac aagcttattg 844
299 atttttttct tcaactaag agttttctaa tcatacgcgt ttttagaata attctacaga 904
301 tatgtccccc aaagattaag atttctctta aacactaaaa agacatgtaa ttatttgta 964
303 gcaaatgggc gtctggcacg cctctgacac ttttctgtca gcagccagga cagcaggtcc 1024
305 cctccttgat gaagcccttc gggcagacca tgtcacctgt ccagcctgc cccaagaagg 1084
307 gacattaagt ggccttctt catatccaaa cacctggctt gaaatgtgat tagccctgta 1144
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311 aactttttta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1244
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315 <211> LENGTH: 231
316 <212> TYPE: PRT
317 <213> ORGANISM: primate
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324 20 25 30
326 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
327 35 40 45
W--> 329 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa see item 10
330 50 55 60
332 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn
333 65 70 75 80
335 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
336 85 90 95
338 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
339 100 105 110
341 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
342 115 120 125
344 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
345 130 135 140

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/265,540D

DATE: 03/27/2001

TIME: 10:50:05

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Output Set: N:\CRF3\03272001\I265540D.raw

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L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:151 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:187 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:187 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:187 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
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L:190 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
M:340 Repeated in SeqNo=2
L:199 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
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L:329 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
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L:329 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:329 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4